

SEQUENCE LISTING

EV 170 405 209 US  
2976-4039US3

<110> KEITH, TIM

<120> NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES AND  
OBESITY

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<140> 09/548,797

<141> 2000-04-13

<150> 60/129,391

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<170> PatentIn Ver. 2.1

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cta cta ctg ctg ctg ctc tgg cca gtg cca ggc gcc ggg gtg ctt caa 96  
Leu Leu Leu Leu Leu Leu Trp Pro Val Pro Gly Ala Gly Val Leu Gln  
20 25 30  
ggt gag gac gcg ggc ggg gtc ccc ctc acc ctg tgc tct gtc ttt act 144  
Gly Glu Asp Ala Gly Gly Val Pro Leu Thr Leu Cys Ser Val Phe Thr  
35 40 45  
cca gga cat atc cct ggg cag cca gtc acc ccg cac tgg gtc ctg gat 192  
Pro Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp  
50 55 60  
gga caa ccc tgg cgc acc gtc agc ctg gag gag ccg gtc tcg aag cca 240  
Gly Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro  
65 70 75 80  
gac atg ggg ctg gtg gcc ctg gag gct gaa ggc cag gag ctc ctg ctt 288  
Asp Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu  
85 90 95  
gag ctg gag aag aac cac agg ctg ctg gcc cca gga tac ata gaa acc 336  
Glu Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr  
100 105 110  
cac tac ggc cca gat ggg cag cca gtg gtg ctg gcc ccc aac cac acg 384  
His Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr  
115 120 125  
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Asp His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp  
130 135 140  
gta gtc ctc tgc acc tgc tct ggg atg agt ggc ctg atc acc ctc agc 480  
Val Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser  
145 150 155 160  
agg aat gcc agc tat tat ctg cgt ccc tgg cca ccc cgg ggc tcc aag 528  
Arg Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys

165								170				175				
gac	ttc	tca	acc	cac	gag	atc	ttt	cgg	atg	gag	cag	ctg	ctc	acc	tgg	576
Asp	Phe	Ser	Thr	His	Glu	Ile	Phe	Arg	Met	Glu	Gln	Leu	Leu	Thr	Trp	
180				185				190								
aaa	gga	acc	tgt	ggc	cac	agg	gat	cct	ggg	aac	aaa	gcg	ggc	atg	acc	624
Lys	Gly	Thr	Cys	Gly	His	Arg	Asp	Pro	Gly	Asn	Lys	Ala	Gly	Met	Thr	
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agc	ctt	cct	ggt	ggt	ccc	cag	agc	agg	ggc	agg	cga	gaa	gcg	cgc	agg	672
Ser	Leu	Pro	Gly	Gly	Pro	Gln	Ser	Arg	Gly	Arg	Arg	Glu	Ala	Arg	Arg	
210				215				220								
acc	cgg	aag	tac	ctg	gaa	ctg	tac	att	gtg	gca	gac	cac	acc	ctg	ttc	720
Thr	Arg	Lys	Tyr	Leu	Glu	Leu	Tyr	Ile	Val	Ala	Asp	His	Thr	Leu	Phe	
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Leu	Thr	Arg	His	Arg	Asn	Leu	Asn	His	Thr	Lys	Gln	Arg	Leu	Leu	Glu	
245				250				255								
gtc	gcc	aac	tac	gtg	gac	cag	ctt	ctc	agg	act	ctg	gac	att	cag	gtg	816
Val	Ala	Asn	Tyr	Val	Asp	Gln	Leu	Leu	Arg	Thr	Leu	Asp	Ile	Gln	Val	
260				265				270								
gcg	ctg	acc	ggc	ctg	gag	gtg	tgg	acc	gag	cgg	gac	cgc	agc	cgc	gtc	864
Ala	Leu	Thr	Gly	Leu	Glu	Val	Trp	Thr	Glu	Arg	Asp	Arg	Ser	Arg	Val	
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acg	cag	gac	gcc	aac	gcc	acg	ctc	tgg	gcc	ttc	ctg	cag	tgg	cgc	cgg	912
Thr	Gln	Asp	Ala	Asn	Ala	Thr	Leu	Trp	Ala	Phe	Leu	Gln	Trp	Arg	Arg	
290				295				300								
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Gly	Leu	Trp	Ala	Gln	Arg	Pro	His	Asp	Ser	Ala	Gln	Leu	Leu	Thr	Gly	
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cgc	gcc	ttc	cag	ggc	gcc	aca	gtg	ggc	ctg	gcg	ccc	gtc	gag	ggc	atg	1008
Arg	Ala	Phe	Gln	Gly	Ala	Thr	Val	Gly	Leu	Ala	Pro	Val	Glu	Gly	Met	
325				330				335								
tgc	cgc	gcc	gag	agc	tcg	gga	ggc	gtg	agc	acg	gac	cac	tcg	gag	ctc	1056
Cys	Arg	Ala	Glu	Ser	Ser	Gly	Gly	Val	Ser	Thr	Asp	His	Ser	Glu	Leu	
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ccc	atc	ggc	gcc	gca	gcc	acc	atg	gcc	cat	gag	atc	ggc	cac	agc	ctc	1104
Pro	Ile	Gly	Ala	Ala	Ala	Thr	Met	Ala	His	Glu	Ile	Gly	His	Ser	Leu	
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ggc	ctc	agc	cac	gac	ccc	gac	ggc	tgc	tgc	gtg	gag	gct	gcg	gcc	gag	1152
Gly	Leu	Ser	His	Asp	Pro	Asp	Gly	Cys	Cys	Val	Glu	Ala	Ala	Ala	Glu	
370				375				380								
tcc	gga	ggc	tgc	gtc	atg	gct	gcg	gcc	acc	ggg	cac	ccg	ttt	ccg	cgc	1200
Ser	Gly	Gly	Cys	Val	Met	Ala	Ala	Ala	Thr	Gly	His	Pro	Phe	Pro	Arg	
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gtg	ttc	agc	gcc	tgc	agc	cgc	cgc	cag	ctg	cgc	gcc	ttc	ttc	cgc	aag	1248
Val	Phe	Ser	Ala	Cys	Ser	Arg	Arg	Gln	Leu	Arg	Ala	Phe	Phe	Arg	Lys	
405				410												

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ccg ccg gcg ctc tgc ggg aac ggc ttc gtg gaa gcg ggc gag gag tgt Pro Pro Ala Leu Cys Gly Asn Gly Phe Val Glu Ala Gly Glu Glu Cys 435 440 445	1344
gac tgc ggc cct ggc cag gag tgc cgc gac ctc tgc tgc ttt gct cac Asp Cys Gly Pro Gly Gln Glu Cys Arg Asp Leu Cys Cys Phe Ala His 450 455 460	1392
aac tgc tcg ctg cgc ccg ggg gcc cag tgc gcc cac ggg gac tgc tgc Asn Cys Ser Leu Arg Pro Gly Ala Gln Cys Ala His Gly Asp Cys Cys 465 470 475 480	1440
gtg cgc tgc ctg ctg aag ccg gct gga gcg ctg tgc cgc cag gcc atg Val Arg Cys Leu Leu Lys Pro Ala Gly Ala Leu Cys Arg Gln Ala Met 485 490 495	1488
ggt gac tgt gac ctc cct gag ttt tgc acg ggc acc tcc tcc cac tgt Gly Asp Cys Asp Leu Pro Glu Phe Cys Thr Gly Thr Ser Ser His Cys 500 505 510	1536
ccc cca gac gtt tac cta ctg gac ggc tca ccc tgt gcc agg ggc agt Pro Pro Asp Val Tyr Leu Leu Asp Gly Ser Pro Cys Ala Arg Gly Ser 515 520 525	1584
ggc tac tgc tgg gat ggc gca tgt ccc acg ctg gag cag cag tgc cag Gly Tyr Cys Trp Asp Gly Ala Cys Pro Thr Leu Glu Gln Gln Cys Gln 530 535 540	1632
cag ctc tgg ggg cct ggc tcc cac cca gct ccc gag gcc tgt ttc cag Gln Leu Trp Gly Pro Gly Ser His Pro Ala Pro Glu Ala Cys Phe Gln 545 550 555 560	1680
gtg gtg aac tct gcg gga gat gct cat gga aac tgc ggc cag gac agc Val Val Asn Ser Ala Gly Asp Ala His Gly Asn Cys Gly Gln Asp Ser 565 570 575	1728
gag ggc cac ttc ctg ccc tgt gca ggg agg gat gcc ctg tgt ggg aag Glu Gly His Phe Leu Pro Cys Ala Gly Arg Asp Ala Leu Cys Gly Lys 580 585 590	1776
ctg cag tgc cag ggt gga aag ccc agc ctg ctc gca ccg cac atg gtg Leu Gln Cys Gln Gly Gly Lys Pro Ser Leu Leu Ala Pro His Met Val 595 600 605	1824
cca gtg gac tct acc gtt cac cta gat ggc cag gaa gtg act tgt cgg Pro Val Asp Ser Thr Val His Leu Asp Gly Gln Glu Val Thr Cys Arg 610 615 620	1872
gga gcc ttg gca ctc ccc agt gcc cag ctg gac ctg ctt ggc ctg ggc Gly Ala Leu Ala Leu Pro Ser Ala Gln Leu Asp Leu Leu Gly Leu Gly 625 630 635 640	1920
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agg cgc tgc agg aag aat gcc ttc cag gag ctt cag cgc tgc ctg act	2016
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660 665 670	
gcc tgc cac agc cac ggg gtt tgc aat agc aac cat aac tgc cac tgt	2064
Ala Cys His Ser His Gly Val Cys Asn Ser Asn His Asn Cys His Cys	
675 680 685	
gct cca ggc tgg gct cca ccc ttc tgt gac aag cca ggc ttt ggt ggc	2112
Ala Pro Gly Trp Ala Pro Pro Phe Cys Asp Lys Pro Gly Phe Gly Gly	
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agc atg gac agt ggc cct gtg cag gct gaa aac cat gac acc ttc ctg	2160
Ser Met Asp Ser Gly Pro Val Gln Ala Glu Asn His Asp Thr Phe Leu	
705 710 715 720	
ctg gcc atg ctc ctc agc gtc ctg ctg cct ctg ctc cca ggg gcc ggc	2208
Leu Ala Met Leu Leu Ser Val Leu Leu Pro Leu Leu Pro Gly Ala Gly	
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ctg gcc tgg tgt tgc tac cga ctc cca gga gcc cat ctg cag cga tgc	2256
Leu Ala Trp Cys Cys Tyr Arg Leu Pro Gly Ala His Leu Gln Arg Cys	
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Ser Trp Gly Cys Arg Arg Asp Pro Ala Cys Ser Gly Pro Lys Asp Gly	
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Pro His Arg Asp His Pro Leu Gly Gly Val His Pro Met Glu Leu Gly	
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Pro Thr Ala Thr Gly Gln Pro Trp Pro Leu Ala Pro Gly Ser Pro Ala	
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Asp His Ile His Asn Ile Tyr Pro Pro Pro Phe Leu Pro Asp Pro Glu	
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aac tct cat gag ccc agc agc cac cct gag aag cct ctg cca gca gtc	2496
Asn Ser His Glu Pro Ser Ser His Pro Glu Lys Pro Leu Pro Ala Val	
820 825 830	
tcg cct gac ccc caa gca gat caa gtc cag atg cca aga tcc tgc ctc	2544
Ser Pro Asp Pro Gln Ala Asp Gln Val Gln Met Pro Arg Ser Cys Leu	
835 840 845	
tgg tga gaggtagctc ctaaaatgaa cagatttaaa gacaggtggc cactgacagc	2600
Trp	
cactccagga acttgaactg caggggcaga gccagtgaat caccggacct ccagcacctg	2660
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<211> 746

<212> PRT

<213> Homo sapiens

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			20					25					30		
Gly	His	Ile	Pro	Gly	Gln	Pro	Val	Thr	Pro	His	Trp	Val	Leu	Asp	Gly
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Gln	Pro	Trp	Arg	Thr	Val	Ser	Leu	Glu	Glu	Pro	Val	Ser	Lys	Pro	Asp
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Met	Gly	Leu	Val	Ala	Leu	Glu	Ala	Glu	Gly	Gln	Glu	Leu	Leu	Leu	Glu
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Leu	Glu	Lys	Asn	His	Arg	Leu	Leu	Ala	Pro	Gly	Tyr	Ile	Glu	Thr	His
				85					90					95	
Tyr	Gly	Pro	Asp	Gly	Gln	Pro	Val	Val	Leu	Ala	Pro	Asn	His	Thr	Asp
			100					105					110		
His	Cys	His	Tyr	Gln	Gly	Arg	Val	Arg	Gly	Phe	Pro	Asp	Ser	Trp	Val
		115					120					125			
Val	Leu	Cys	Thr	Cys	Ser	Gly	Met	Ser	Gly	Leu	Ile	Thr	Leu	Ser	Arg
		130				135					140				
Asn	Ala	Ser	Tyr	Tyr	Leu	Arg	Pro	Trp	Pro	Pro	Arg	Gly	Ser	Lys	Asp
145					150					155					160

Phe	Ser	Thr	His	Glu	Ile	Phe	Arg	Met	Glu	Gln	Leu	Leu	Thr	Trp	Lys	165	170	175
Gly	Thr	Cys	Gly	His	Arg	Asp	Pro	Gly	Asn	Lys	Ala	Gly	Met	Thr	Ser	180	185	190
Leu	Pro	Gly	Gly	Pro	Gln	Ser	Arg	Gly	Arg	Arg	Glu	Ala	Arg	Arg	Thr	195	200	205
Arg	Lys	Tyr	Leu	Glu	Leu	Tyr	Ile	Val	Ala	Asp	His	Thr	Leu	Phe	Leu	210	215	220
Thr	Arg	His	Arg	Asn	Leu	Asn	His	Thr	Lys	Gln	Arg	Leu	Leu	Glu	Val	225	230	235
Ala	Asn	Tyr	Val	Asp	Gln	Leu	Leu	Arg	Thr	Leu	Asp	Ile	Gln	Val	Ala	245	250	255
Leu	Thr	Gly	Leu	Glu	Val	Trp	Thr	Glu	Arg	Asp	Arg	Ser	Arg	Val	Thr	260	265	270
Gln	Asp	Ala	Asn	Ala	Thr	Leu	Trp	Ala	Phe	Leu	Gln	Trp	Arg	Arg	Gly	275	280	285
Leu	Trp	Ala	Gln	Arg	Pro	His	Asp	Ser	Ala	Gln	Leu	Leu	Thr	Gly	Arg	290	295	300
Ala	Phe	Gln	Gly	Ala	Thr	Val	Gly	Leu	Ala	Pro	Val	Glu	Gly	Met	Cys	305	310	315
Arg	Ala	Glu	Ser	Ser	Gly	Gly	Val	Ser	Thr	Asp	His	Ser	Glu	Leu	Pro	325	330	335
Ile	Gly	Ala	Ala	Ala	Thr	Met	Ala	His	Glu	Ile	Gly	His	Ser	Leu	Gly	340	345	350
Leu	Ser	His	Asp	Pro	Asp	Gly	Cys	Cys	Val	Glu	Ala	Ala	Ala	Glu	Ser	355	360	365
Gly	Gly	Cys	Val	Met	Ala	Ala	Ala	Thr	Gly	His	Pro	Phe	Pro	Arg	Val	370	375	380
Phe	Ser	Ala	Cys	Ser	Arg	Arg	Gln	Leu	Arg	Ala	Phe	Phe	Arg	Lys	Gly	385	390	395
Gly	Gly	Ala	Cys	Leu	Ser	Asn	Ala	Pro	Asp	Pro	Gly	Leu	Pro	Val	Pro	405	410	415
Pro	Ala	Leu	Cys	Gly	Asn	Gly	Phe	Val	Glu	Ala	Gly	Glu	Glu	Cys	Asp	420	425	430
Cys	Gly	Pro	Gly	Gln	Glu	Cys	Arg	Asp	Leu	Cys	Cys	Phe	Ala	His	Asn	435	440	445
Cys	Ser	Leu	Arg	Pro	Gly	Ala	Gln	Cys	Ala	His	Gly	Asp	Cys	Cys	Val	450	455	460
Arg	Cys	Leu	Leu	Lys	Pro	Ala	Gly	Ala	Leu	Cys	Arg	Gln	Ala	Met	Gly	465	470	475
Asp	Cys	Asp	Leu	Pro	Glu	Phe	Cys	Thr	Gly	Thr	Ser	Ser	His	Cys	Pro			

485										490										495									
Pro	Asp	Val	Tyr	Leu	Leu	Asp	Gly	Ser	Pro	Cys	Ala	Arg	Gly	Ser	Gly														
			500					505					510																
Tyr	Cys	Trp	Asp	Gly	Ala	Cys	Pro	Thr	Leu	Glu	Gln	Gln	Cys	Gln	Gln														
		515					520					525																	
Leu	Trp	Gly	Pro	Asp	Gly	Gln	Glu	Val	Thr	Cys	Arg	Gly	Ala	Leu	Ala														
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Gly	Thr	Gln	Cys	Gly	Pro	Arg	Met	Val	Cys	Gln	Ser	Arg	Arg	Cys	Arg														
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Lys	Asn	Ala	Phe	Gln	Glu	Leu	Gln	Arg	Cys	Leu	Thr	Ala	Cys	His	Ser														
		580						585					590																
His	Gly	Val	Cys	Asn	Ser	Asn	His	Asn	Cys	His	Cys	Ala	Pro	Gly	Trp														
		595					600					605																	
Ala	Pro	Pro	Phe	Cys	Asp	Lys	Pro	Gly	Phe	Gly	Gly	Ser	Met	Asp	Ser														
	610					615					620																		
Gly	Pro	Val	Gln	Ala	Glu	Asn	His	Asp	Thr	Phe	Leu	Leu	Ala	Met	Leu														
	625				630				635					640															
Leu	Ser	Val	Leu	Leu	Pro	Leu	Leu	Pro	Gly	Ala	Gly	Leu	Ala	Trp	Cys														
			645					650						655															
Cys	Tyr	Arg	Leu	Pro	Gly	Ala	His	Leu	Gln	Arg	Cys	Ser	Trp	Gly	Cys														
		660						665					670																
Arg	Arg	Asp	Pro	Ala	Cys	Ser	Gly	Pro	Lys	Asp	Gly	Pro	His	Arg	Asp														
		675					680					685																	
His	Pro	Leu	Gly	Gly	Val	His	Pro	Met	Glu	Leu	Gly	Pro	Thr	Ala	Thr														
		690				695					700																		
Gly	Gln	Pro	Trp	Pro	Leu	Asp	Pro	Glu	Asn	Ser	His	Glu	Pro	Ser	Ser														
	705				710				715					720															
His	Pro	Glu	Lys	Pro	Leu	Pro	Ala	Val	Ser	Pro	Asp	Pro	Gln	Ala	Asp														
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Gln	Val	Gln	Met	Pro	Arg	Ser	Cys	Leu	Trp																				
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<211> 787

<212> PRT

<213> Homo sapiens

<400> 5

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	20		25		30	
Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly	35		40		45	
Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp	50		55		60	
Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu	65		70		75	80
Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His		85		90		95
Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp		100		105		110
His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val		115		120		125
Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser Arg		130		135		140
Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp		145		150		155
Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys		165		170		175
Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser		180		185		190
Leu Pro Gly Gly Pro Gln Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr		195		200		205
Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu		210		215		220
Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val		225		230		235
Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala		245		250		255
Leu Thr Gly Leu Glu Val Trp Thr Glu Arg Asp Arg Ser Arg Val Thr		260		265		270
Gln Asp Ala Asn Ala Thr Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly		275		280		285
Leu Trp Ala Gln Arg Pro His Asp Ser Ala Gln Leu Leu Thr Gly Arg		290		295		300
Ala Phe Gln Gly Ala Thr Val Gly Leu Ala Pro Val Glu Gly Met Cys		305		310		315
Arg Ala Glu Ser Ser Gly Gly Val Ser Thr Asp His Ser Glu Leu Pro		325		330		335
Ile Gly Ala Ala Ala Thr Met Ala His Glu Ile Gly His Ser Leu Gly		340		345		350



Leu Ser His Asp Pro Asp Gly Cys Cys Val Glu Ala Ala Ala Glu Ser  
 355 360 365  
 Gly Gly Cys Val Met Ala Ala Ala Thr Gly His Pro Phe Pro Arg Val  
 370 375 380  
 Phe Ser Ala Cys Ser Arg Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly  
 385 390 395 400  
 Gly Gly Ala Cys Leu Ser Asn Ala Pro Asp Pro Gly Leu Pro Val Pro  
 405 410 415  
 Pro Ala Leu Cys Gly Asn Gly Phe Val Glu Ala Gly Glu Glu Cys Asp  
 420 425 430  
 Cys Gly Pro Gly Gln Glu Cys Arg Asp Leu Cys Cys Phe Ala His Asn  
 435 440 445  
 Cys Ser Leu Arg Pro Gly Ala Gln Cys Ala His Gly Asp Cys Cys Val  
 450 455 460  
 Arg Cys Leu Leu Lys Pro Ala Gly Ala Leu Cys Arg Gln Ala Met Gly  
 465 470 475 480  
 Asp Cys Asp Leu Pro Glu Phe Cys Thr Gly Thr Ser Ser His Cys Pro  
 485 490 495  
 Pro Asp Val Tyr Leu Leu Asp Gly Ser Pro Cys Ala Arg Gly Ser Gly  
 500 505 510  
 Tyr Cys Trp Asp Gly Ala Cys Pro Thr Leu Glu Gln Gln Cys Gln Gln  
 515 520 525  
 Leu Trp Gly Pro Gly Ser His Pro Ala Pro Glu Ala Cys Phe Gln Val  
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 Val Asn Ser Ala Gly Asp Ala His Gly Asn Cys Gly Gln Asp Ser Glu  
 545 550 555 560  
 Gly His Phe Leu Pro Cys Ala Gly Arg Asp Ala Leu Cys Gly Lys Leu  
 565 570 575  
 Gln Cys Gln Gly Gly Lys Pro Ser Leu Leu Ala Pro His Met Val Pro  
 580 585 590  
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Gly Pro Lys Asp Gly Pro His Arg Asp His Pro Leu Gly Gly Val His  
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<223> Description of Artificial Sequence: Primer

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<210> 9

<211> 22

<212> DNA

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<223> Description of Artificial Sequence: Primer

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aatatcatgc accatgaccc ac

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<210> 10

<211> 22

<212> DNA

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<223> Description of Artificial Sequence: Primer

<400> 10

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22

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 11

ggagcttatc ctggattatc ta

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<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 12

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22

<210> 13

<211> 22

<212> DNA

<213> Artificial Sequence

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<210> 14  
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<210> 15  
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<210> 16  
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<223> Description of Artificial Sequence: Primer

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<210> 18  
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<400> 18  
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<210> 19  
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ataaccagat ggctgtgggt ca 22

<210> 21  
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<223> Description of Artificial Sequence: Primer

<400> 21  
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<210> 22  
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<223> Description of Artificial Sequence: Primer

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<223> Description of Artificial Sequence: Primer

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gcattggggg aagccaggac at

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<223> Description of Artificial Sequence: Primer

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<210> 25

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<212> DNA

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<223> Description of Artificial Sequence: Primer

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22

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22

<210> 27

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<400> 27

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<210> 28

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 28  
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<210> 29  
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<210> 30  
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<223> Description of Artificial Sequence: Primer

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<210> 31  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 31  
cgacatttag gtgacact 18

<210> 32  
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<223> Description of Artificial Sequence: Synthetic  
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<210> 33  
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<220>  
<223> Description of Artificial Sequence: Synthetic

linker adapter

<400> 33  
gtggtgaaga c 11

<210> 34  
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linker

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<210> 35  
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linker

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<223> Description of Artificial Sequence: Synthetic  
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<400> 36  
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<210> 37  
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<223> Description of Artificial Sequence: Synthetic  
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<400> 37  
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<210> 38  
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<223> Description of Artificial Sequence: Synthetic  
linker

<400> 38

cctacggaat tctcactcag c

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<210> 39

<211> 23

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<223> Description of Artificial Sequence: Synthetic  
linker

<400> 39

ttgctgagtg agaattccgt agg

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<210> 40

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<212> DNA

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<223> Description of Artificial Sequence: Synthetic  
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<400> 40

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<210> 41

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<212> DNA

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<223> Description of Artificial Sequence: Synthetic  
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<400> 41

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<210> 42

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<212> DNA

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<223> Description of Combined DNA/RNA Molecule: Synthetic  
oligonucleotide

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide



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<223> Description of Combined DNA/RNA Molecule: Synthetic  
oligonucleotide

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oligonucleotide

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<223> Description of Combined DNA/RNA Molecule: Synthetic  
oligonucleotide

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oligonucleotide

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<400> 45  
cuacuacuac uagaatccga attcctggtc agc 33

<210> 46  
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<223> Description of Artificial Sequence: Synthetic peptide

<400> 46

Thr Met Ala His Glu Ile Gly His Ser Leu Gly Leu Ser His Asp Pro  
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Asp

<210> 47

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 47

Cys Cys Phe Ala His Asn Cys Ser Leu Arg Pro Gly Ala Gln Cys Ala  
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His Gly Asp Cys Cys Val Arg Cys Leu Leu Lys Pro Ala Gly Ala Leu  
20 25 30

Cys Arg Gln Ala Met Gly Asp Cys Asp Leu Pro Glu Phe Cys Thr Gly  
35 40 45

Thr Ser Ser His Cys Pro Pro  
50 55

<210> 48

<211> 11

<212> PRT

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<210> 166  
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<220>  
<223> Description of Artificial Sequence: Primer

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<210> 167  
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<220>

<223> Description of Artificial Sequence: Primer

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<223> Description of Artificial Sequence: Primer

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<223> Description of Artificial Sequence: Primer

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<223> Description of Artificial Sequence: Primer

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